Fig. 1A

Sequence ID No. 4

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GGTCGGCAGGACATCAGCATTATTAATTCTAGGAAACTCATTATGGATAACAAGGAAACT    18
                                          M  D  N  K  E  T      6

AACGGAGAGCTAGAGCAGTCTGATGAGGCCGATCCGTCCGGTCAAAACCTTGATGATGGG   78
 N  G  E  L  E  Q  S  D  E  A  D  P  S  G  Q  N  L  D  D  G   26

GAAACCGATAGCAAACAAGAAGAGAATCTCATCAACGTTAGCCCGCCAAAAACACCGCCA  138
 E  T  D  S  K  Q  E  E  N  L  I  N  V  S  P  P  K  T  P  P   46

GGTCCTCCTCCTCCTCTAAAGAATGGAGGAAGGGGTCAGAAACCGCCCAAAATCCCAATA  198
 G  P  P  P  P  L  K  N  G  G  R  G  Q  K  P  P  K  I  P  I   66

TGTCATCAAAATGGAAAGCTCCCCAAGGAAGTTGAATGGACAGAAGACAGAGGCGAAGAC  258
 C  H  Q  N  G  K  L  P  K  E  V  E  W  T  E  D  R  G  E  D   86

AGAAAGGATAGTCTCACTCTTCAATCAAAGCTAGATCACGGGGCATACACGGATGAGAAA  318
 R  K  D  S  L  T  L  Q  S  K  L  D  H  G  A  Y  T  D  E  K  106
          ▲

CAGGATCTTCTAACATATCTTGACCGTCACGGCATCAACAGTCCAGTCAAGCTAACACCA  378
 Q  D  L  L  T  Y  L  D  R  H  G  I  N  S  P  V  K  L  T  P  126

GATGAAACTGGAGGGAGCAGTGCTTTGGATATTCTTGGGATTATTGAAGAGAGGGACACT  438
 D  E  T  G  G  S  S  A  L  D  I  L  G  I  I  E  E  R  D  T  146

GGTGCACTAGGCTCTGATCCCTCATCCACTATGCAGGCCATGGCTAAACCTGTAGGCTTT  498
 G  A  L  G  S  D  P  S  S  T  M  Q  A  M  A  K  P  V  G  F  166

CTGCAGAGGCAGCTATGGACTGTCCTCCAACCTTCAGACAATAGACTCTCCATGAAACTT  558
 L  Q  R  Q  L  W  T  V  L  Q  P  S  D  N  R  L  S  M  K  L  186
                                                ●

TTCGGAAGCAAGAAAGGGTTACAAAAGGAAAAATATCGGCTGAGGAAGGCGGGGGTTCTT  618
 F  G  S  K  K  G  L  Q  K  E  K  Y  R  L  R  K  A  G  V  L  206
       ●

                                        S1
ATCATTCATCCATGTAGTCATTTCAGATTTTACTGGGATCTACTGATGCTGTGCCTGATC  678
 I  I  H  P  C  S  H  F  R  F  Y  W  D  L  L  M  L  C  L  I  226

ATGGCAAACGTCATCCTCCTACCCGTCGTCATTACTTTCTTCCACAACAAGGACATGAGT  738
 M  A  N  V  I  L  L  P  V  V  I  T  F  F  H  N  K  D  M  S  246

                                        S2
ACGGGTTGGCTCATCTTTAATTGCTTCTCAGATACCTTCTTCATTCTCGATCTCATCTGC  798
 T  G  W  L  I  F  N  C  F  S  D  T  F  F  I  L  D  L  I  C  266

AACTTTCGGACCGGCATCATGAATCCGAAGTCGGCCGAACAGGTGATCCTCAACCCCCGT  858
 N  F  R  T  G  I  M  N  P  K  S  A  E  Q  V  I  L  N  P  R  286

                                        S3
CAAATCGCCTATCATTATCTCCGTTCATGGTTCATCATCGATCTCGTGTCTTCCATCCCC  918
 Q  I  A  Y  H  Y  L  R  S  W  F  I  I  D  L  V  S  S  I  P  306
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ATGGACTACATCTTCCTCCTCGCTGGCGGCCAGAACCGTCACTTCCTCGAGGTGTCCCGA   978
 M  D  Y  I  F  L  L  A  G  G  Q  N  R  H  F  L  E  V  S  R    326

                                  S4
GCCCTCAAGATACTGCGCTTTGCCAAGCTCCTCAGTCTTCTTCGACTCCTGCGTCTGTCC  1038
 A  L  K  I  L  R  F  A  K  L  L  S  L  L  R  L  L  R  L  S    346

AGGCTCATGCGGTTCGTCAGTCAATGGGAACAGGCCTTCAACGTAGCCAATGCCGTCATC  1098
 R  L  M  R  F  V  S  Q  W  E  Q  A  F  N  V  A  N  A  V  I    366

                                  S5
CGGATCTGTAATCTAGTGTGTATGATGCTTCTGATTGGCCATTGGAATGGCTGCCTTCAA  1158
 R  I  C  N  L  V  C  M  M  L  L  I  G  H  W  N  G  C  L  Q    386

TATCTCGTGCCCATGCTGCAAGAATACCCCGACCAATCATGGGTCGCCATTAATGGCCTT  1218
 Y  L  V  P  M  L  Q  E  Y  P  D  Q  S  W  V  A  I  N  G  L    406

                                                  Pore
GAGCACGCTCATTGGTGGGAGCAGTATACATGGGCACTCTTCAAAGCCCTTTCGCACATG  1278
 E  H  A  H  W  W  E  Q  Y  T  W  A  L  F  K  A  L  S  H  M    426

CTCTGTATCGGGTACGGCAAGTTCCCCCCTCAAAGCATCACCGATGTCTGGCTAACGATT  1338
 L  C  I  G  Y  G  K  F  P  P  Q  S  I  T  D  V  W  L  T  I    446

                                  S6
GTCAGTATGGTGTCCGGTGCGACCTGCTTCGCCCTGTTCATCGGACACGCTACCAATCTC  1398
 V  S  M  V  S  G  A  T  C  F  A  L  F  I  G  H  A  T  N  L    466

ATCCAGTCCATGGACTCCTCCAGCAGGCAATACCGTGAGAAGTTGAAACAAGTTGAAGAG  1458
 I  Q  S  M  D  S  S  S  R  Q  Y  R  E  K  L  K  Q  V  E  E    486

TACATGCAGTATCGCAAGCTACCGTCCCACCTACGAAACAAGATCCTCGATTACTACGAG  1518
 Y  M  Q  Y  R  K  L  P  S  H  L  R  N  K  I  L  D  Y  Y  E    506

TACCGATACCGAGGAAAGATGTTTGATGAGAGGCATATCTTTCGAGAAGTGTCGGAGAGT  1578
 Y  R  Y  R  G  K  M  F  D  E  R  H  I  F  R  E  V  S  E  S    526

ATACGACAGGATGTCGCAAACTACAATTGTCGCGACCTGGTCGCATCCGTCCCTTTCTTC  1638
 I  R  Q  D  V  A  N  Y  N  C  R  D  L  V  A  S  V  P  F  F    546

GTCGGTGCCGACTCAAACTTCGTCACCCGTGTGGTGACGCTGCTCGAATTCGAGGTCTTC  1698
 V  G  A  D  S  N  F  V  T  R  V  V  T  L  L  E  F  E  V  F    566

CAACCCGCTGACTATGTTATACAGGAAGGTACTTTCGGTGATCGCATGTTCTTCATCCAG  1758
 Q  P  A  D  Y  V  I  Q  E  G  T  F  G  D  R  M  F  F  I  Q    586

CAGGGCATCGTCGACATCATCATGTCCGACGGCGTCATCGCCACGTCACTCAGTGACGGC  1818
 Q  G  I  V  D  I  I  M  S  D  G  V  I  A  T  S  L  S  D  G    606

                                  cNMP binding site
TCATATTTTGGCGAAATCTGCCTGCTTACCCGTGAGCGCCGCGTGGCATCGGTGAAGTGC  1878
 S  Y  F  G  E  I  C  L  L  T  R  E  R  R  V  A  S  V  K  C    626

GAGACCTACTGCACGCTCTTCTCGCTCTCCGTCCAGCATTTCAACCAAGTGCTCGACGAG  1938
 E  T  Y  C  T  L  F  S  L  S  V  Q  H  F  N  Q  V  L  D  E    646
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0960503-080700

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AAGGAATCGAGCAAGCTGAAATCCCGCCTAGAGAGCCCGACGATCAGGGACACTGCCCCT   2058
 K  E  S  S  K  L  K  S  R  L  E  S  P  T  I  R  D  T  A  P     686

CTCTTTCCGATCCCACCTGATACACCGTCTTTCGTCACCGACATCGAAAAGAACCGGTTC   2118
 L  F  P  I  P  P  D  T  P  S  F  V  T  D  I  E  K  N  R  F     706

TTTGGCGACGACACGGACGATGTACACATCAGGACCCGAGTCGACGTCGAGCGTGGTTCG   2178
 F  G  D  D  T  D  D  V  H  I  R  T  R  V  D  V  E  R  G  S     726

CATGAAAACGTCATCGCCATCATGGATGGGAGTTTATCCGACCTCAGGATGGAAAACGAA   2238
 H  E  N  V  I  A  I  M  D  G  S  L  S  D  L  R  M  E  N  E     746

ATCCAAGCCCGTAAATCGTCTAGCGGAAAACGGAGGAAATTCCAGCAACAAACAACCGAA   2298
 I  Q  A  R  K  S  S  S  G  K  R  R  K  F  Q  Q  Q  T  T  E     766

CTATGACGACTTGAAACAAACAATGATGGACGCTTACAATTTCCAGTGATTCAATACTTA   2358
 L  -                                                           767

CGCAATGCAGACATTAGCTTTTGTACCTGATTGTTTAGAATGTATTGAATTTGTAGATCA   2418
GTCCGGCAAATAAGAAAGCATAATTTGGAATTTCTTTCATTGAGGAAGTACTGAAAACAA   2478
TGTGATAGCAGCCGGTAGAAATTTCTTGTCCATTATCGAGGCTATATTTTTCGCGCTTTC   2538
TTACGAAGTAAATGAAAGGATCAATTAAATTATTGTTCTTTGTCTCGTGCGCTTTGTATC   2598
TGATGCCGAAAAGGAATGAAACGTGATTAGAACAGTAATCGATTGAACTACAGAAGTCTT   2658
TTCAAAATGTTGAATGTATGAAGGAGGAGGGGAAGGTTTGATATATGCAAAGAAATGGA    2718
GAAATATTTTTGTAAATTTATCTAGAATGGTACTATTGATGCTGGAAAGGTGTTGAAGTT   2778
GTCCAATATTGTGTCAAATCACCAACTATTTGACATTTGTCTTTTTC                2825
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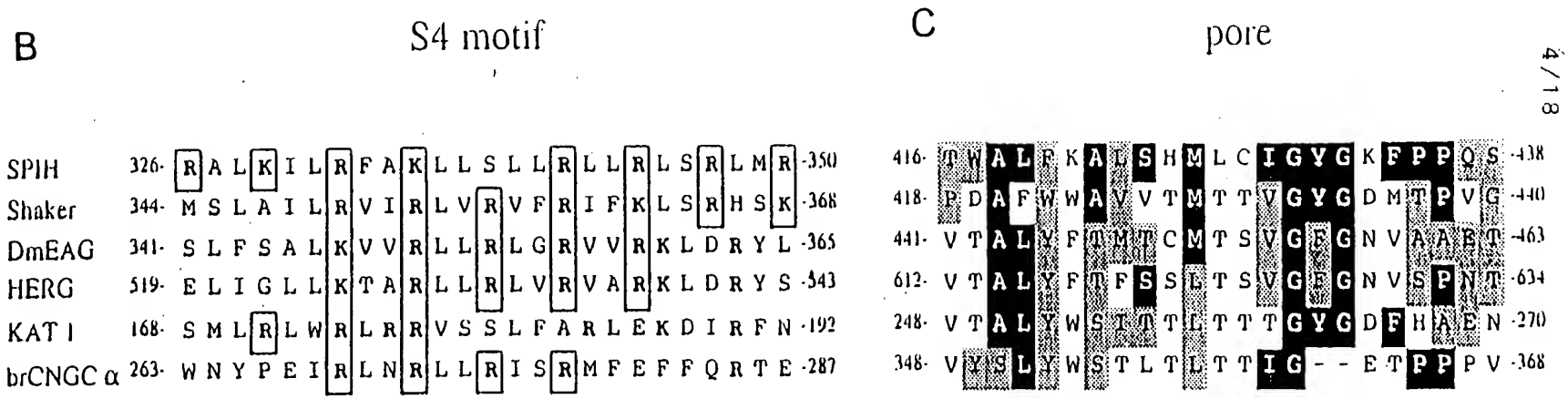
00/780 2850h960

Fig. 1B, 1C



00ZT80°2850h960

cNMP binding domain

Fig. 1D

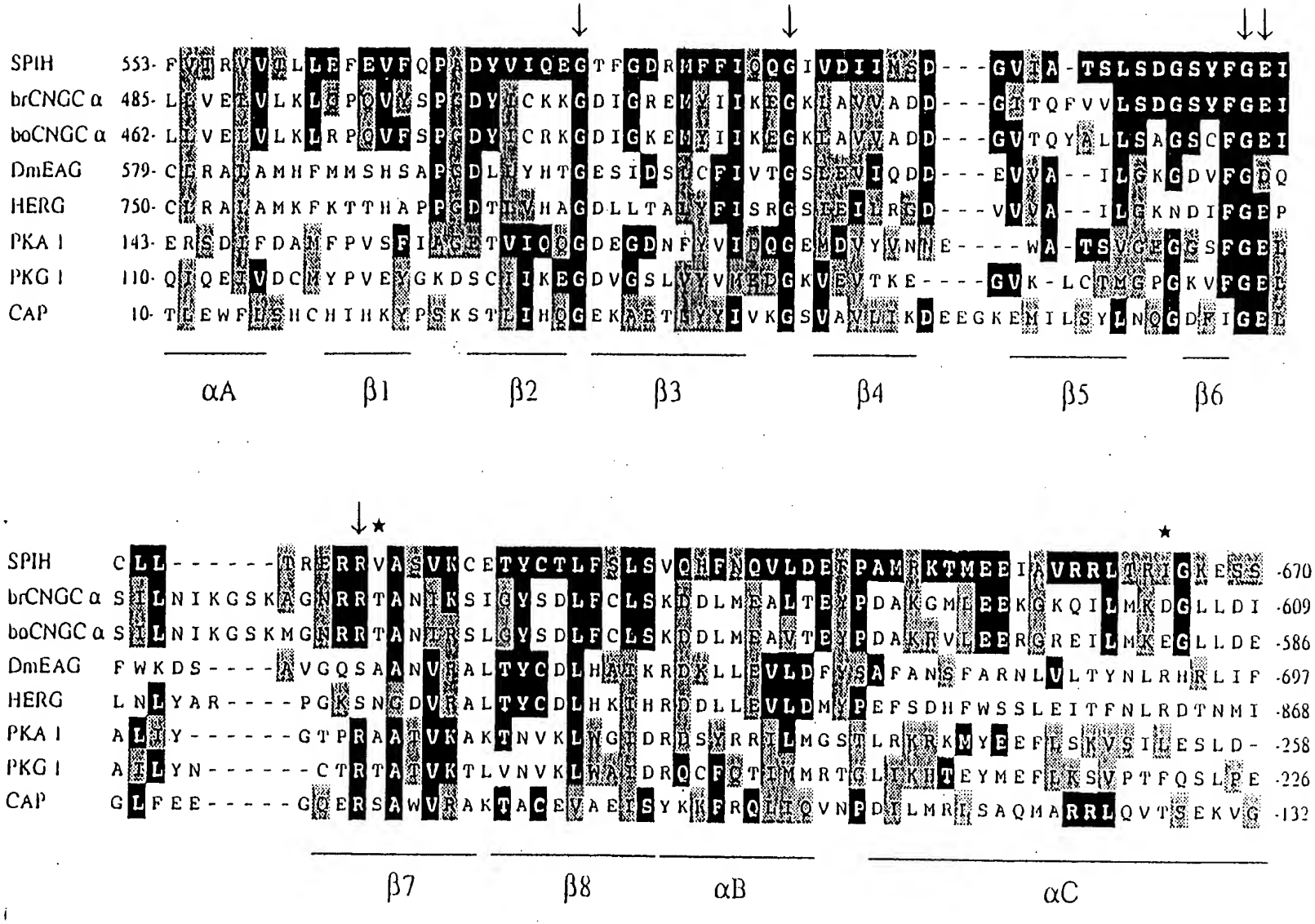


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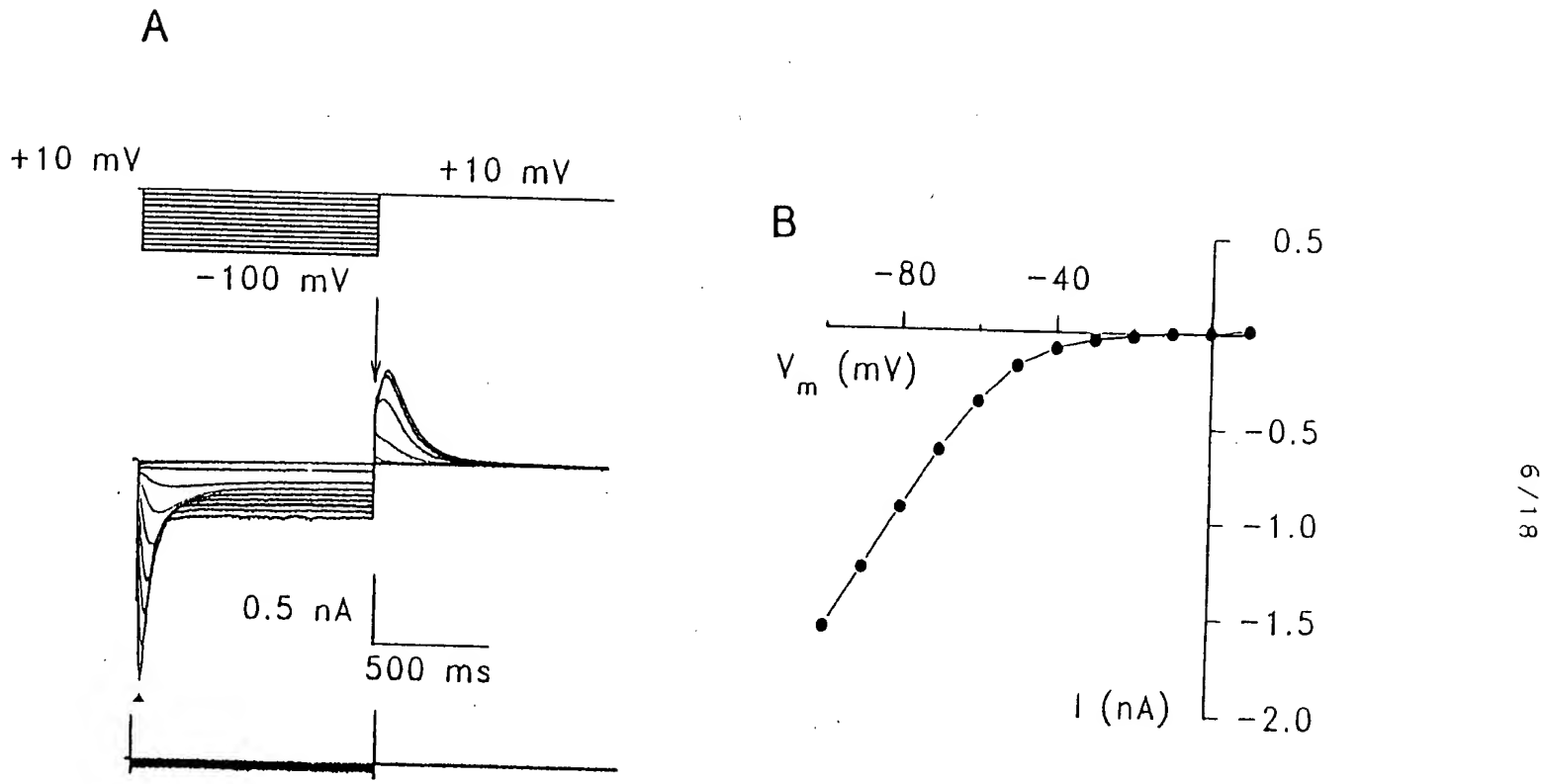
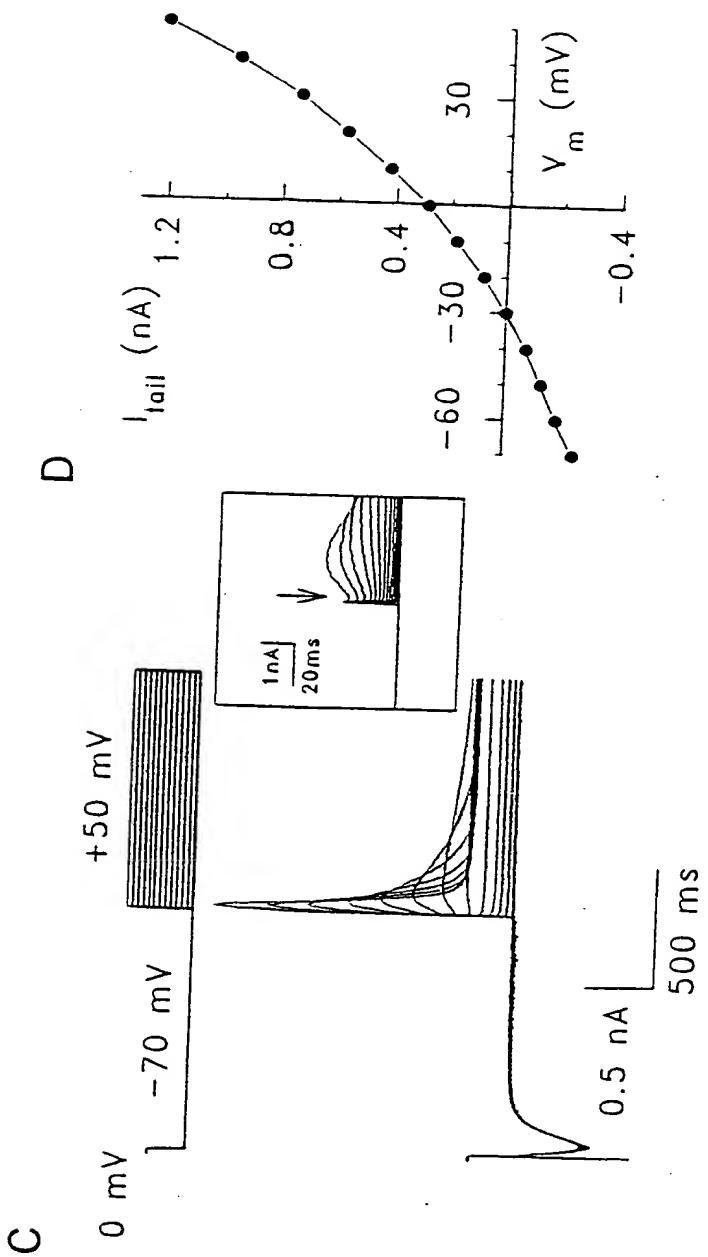
Fig. 2A, 2B



Fig, 2C, 2D


C
0 mV
+50 mV
-70 mV
1nA
20ms
0.5 nA
500 ms
D
I_{tail} (nA)
1.2
0.8
0.4
-0.4
30
-30
-60
V_m (mV)

Fig, 2E, 2F

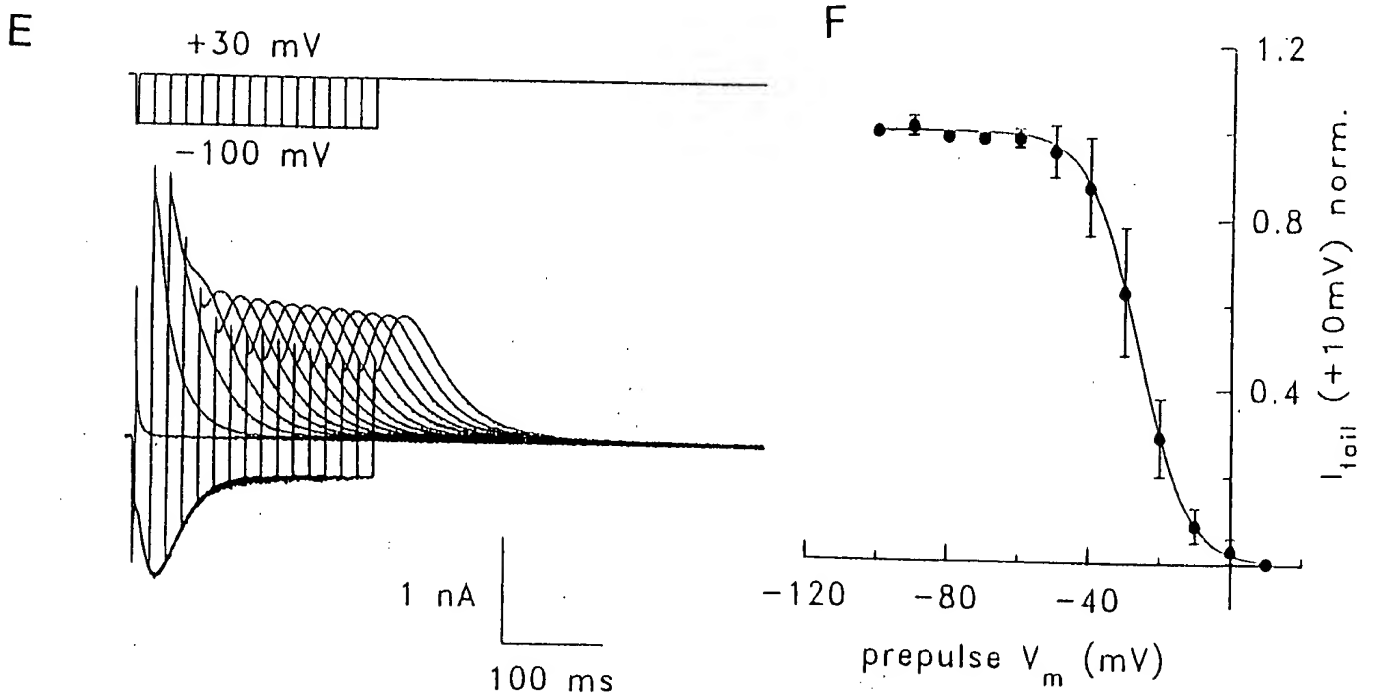
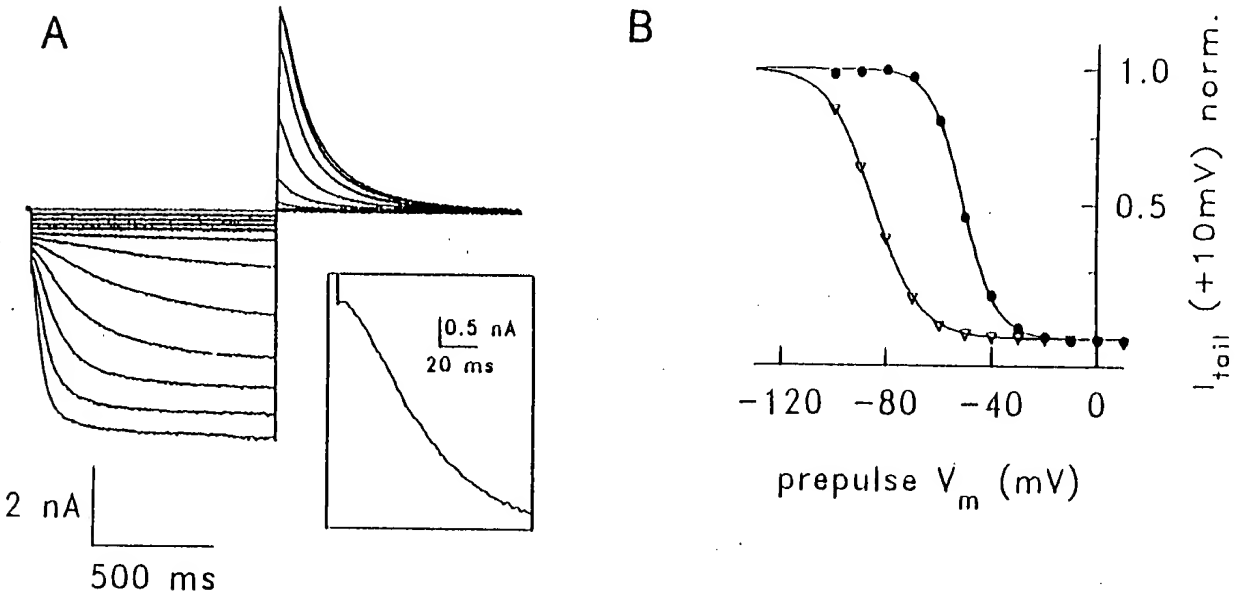
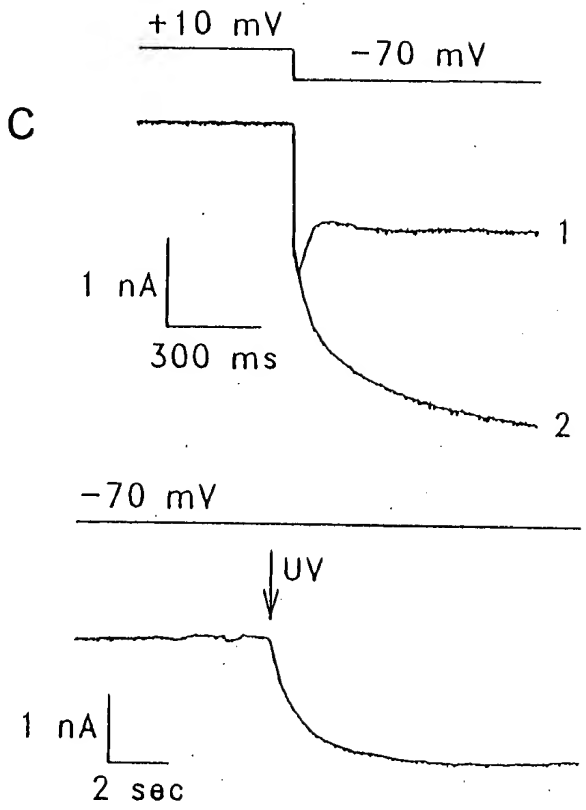

E
+30 mV
−100 mV
1 nA
100 ms
F
1.2
0.8
0.4
I_{tail} (+10mV) norm.
−120
−80
−40
prepulse V_m (mV)

Fig. 3A, 3B



09640582.081700

Fig. 3C, 3D


+10 mV
−70 mV
C
1
1 nA
300 ms
2
−70 mV
UV
1 nA
2 sec

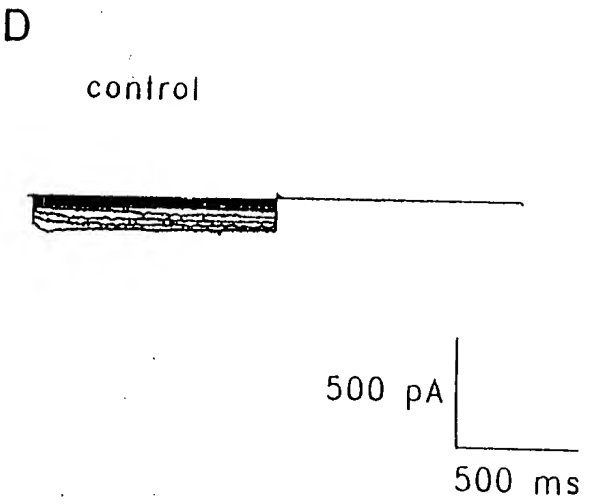
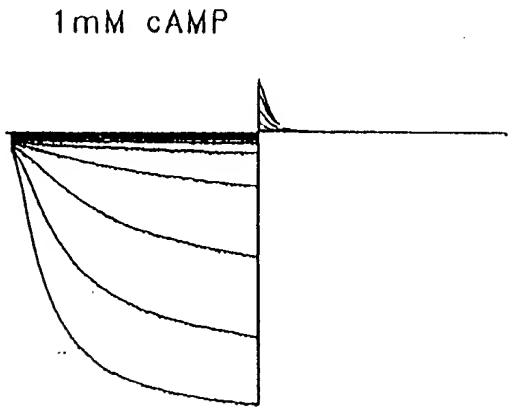
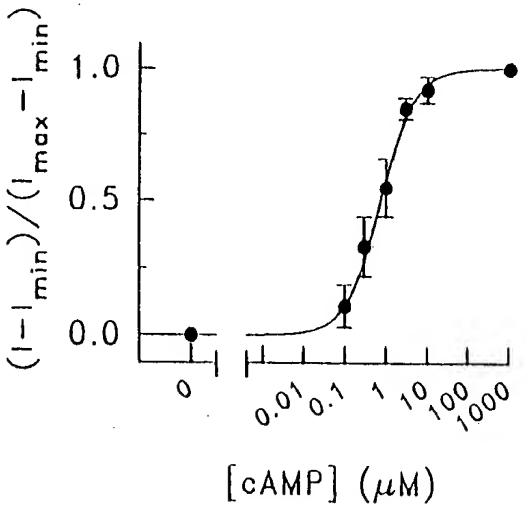

D
control
500 pA
500 ms

Fig. 3E, 3F

E



F



09640582 . 081700

Fig. 4

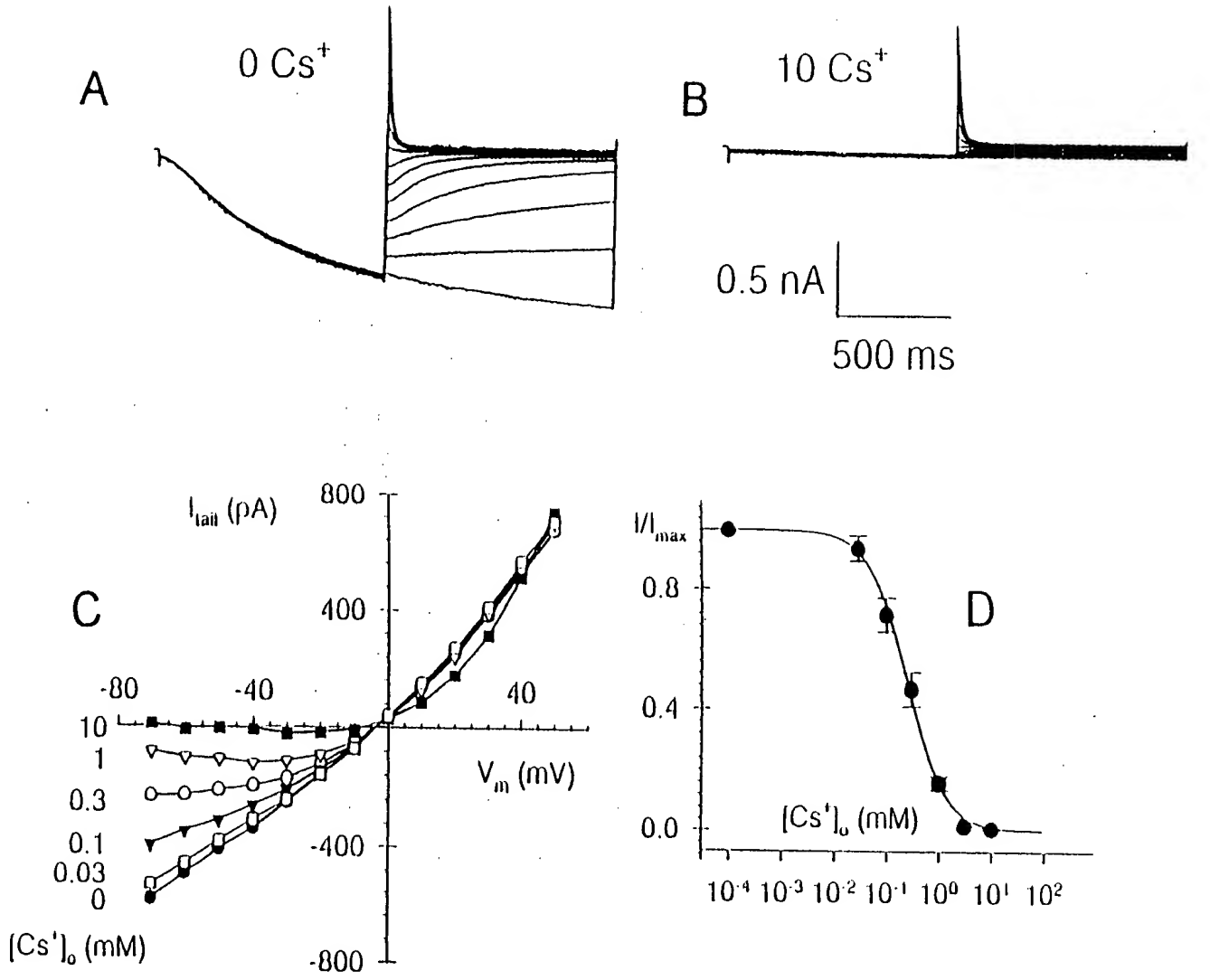

A
0 Cs+
B
10 Cs+
0.5 nA
500 ms
C
Itail (pA)
800
400
-400
-800
-80
-40
40
Vm (mV)
10
1
0.3
0.1
0.03
0
[Cs+]o (mM)
D
I/Imax
0.8
0.4
0.0
[Cs+]o (mM)
10-4 10-3 10-2 10-1 100 101 102

Fig. 4E

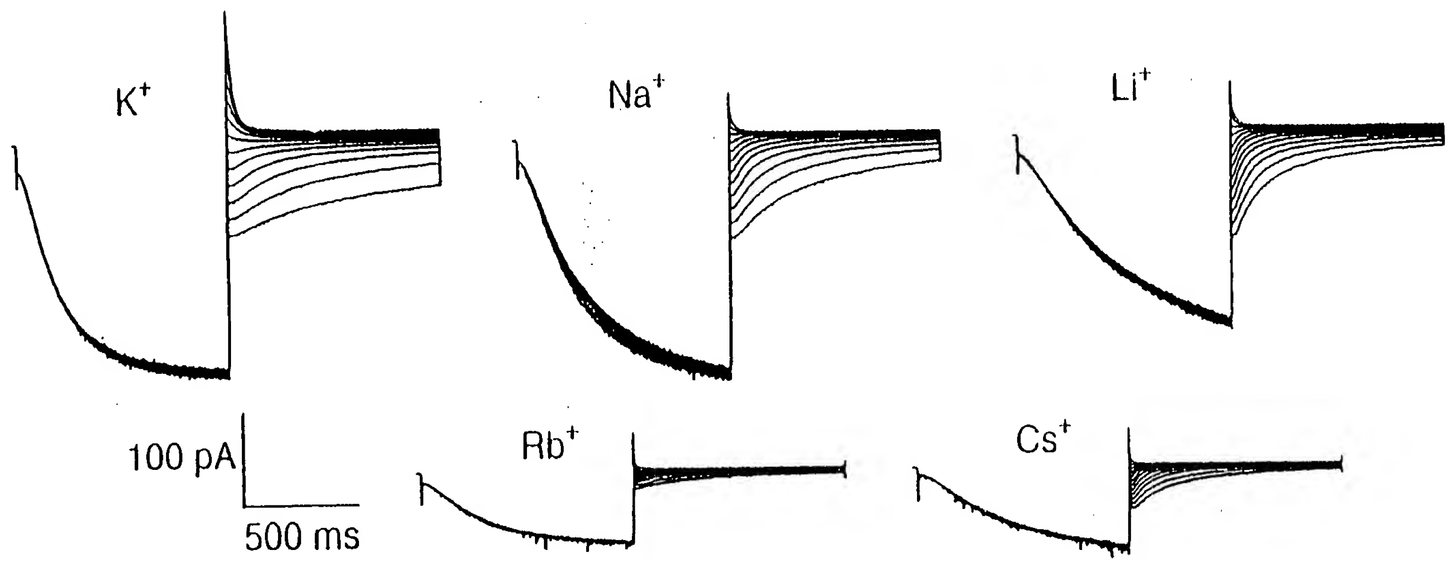


Fig. 4F

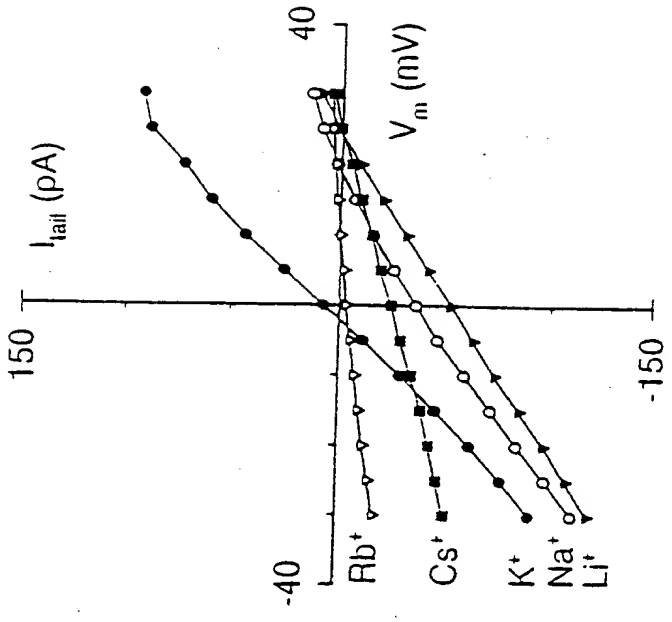


Fig. 4G

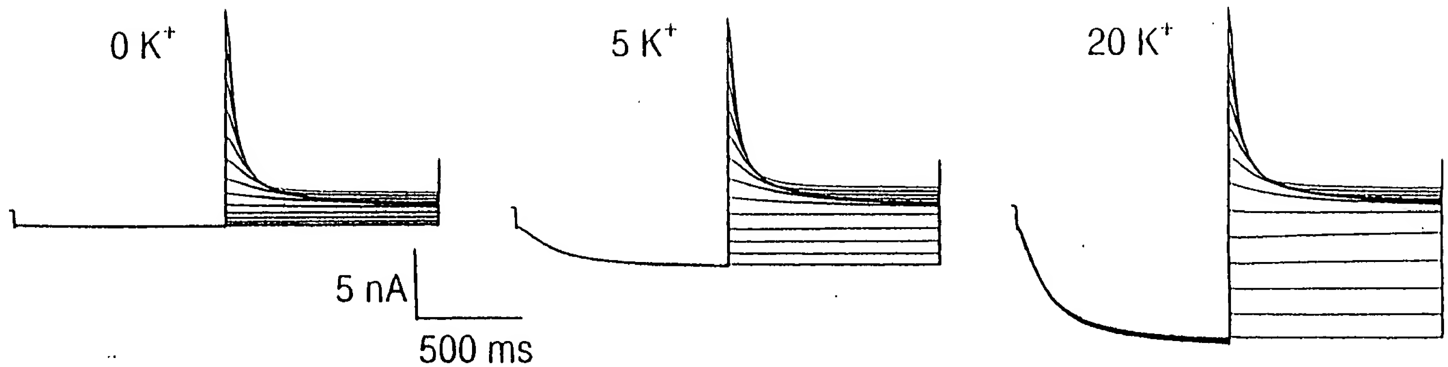


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Fig. 4H

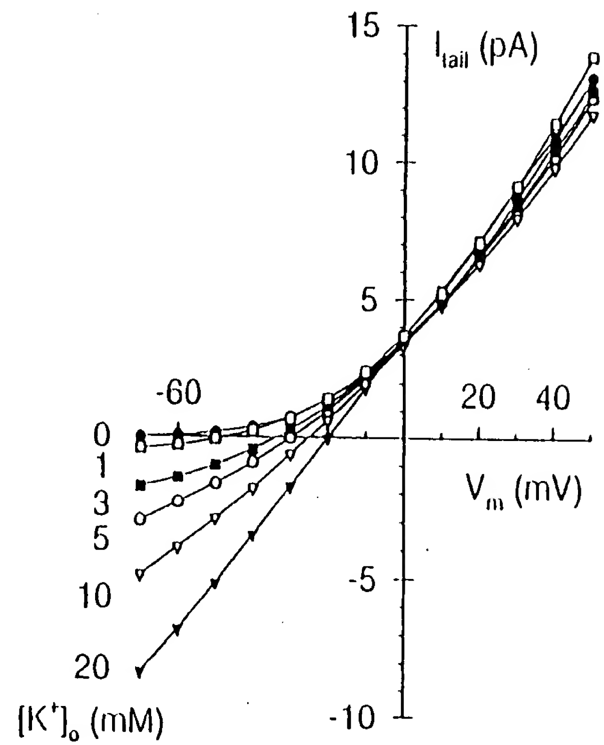

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Fig. 5

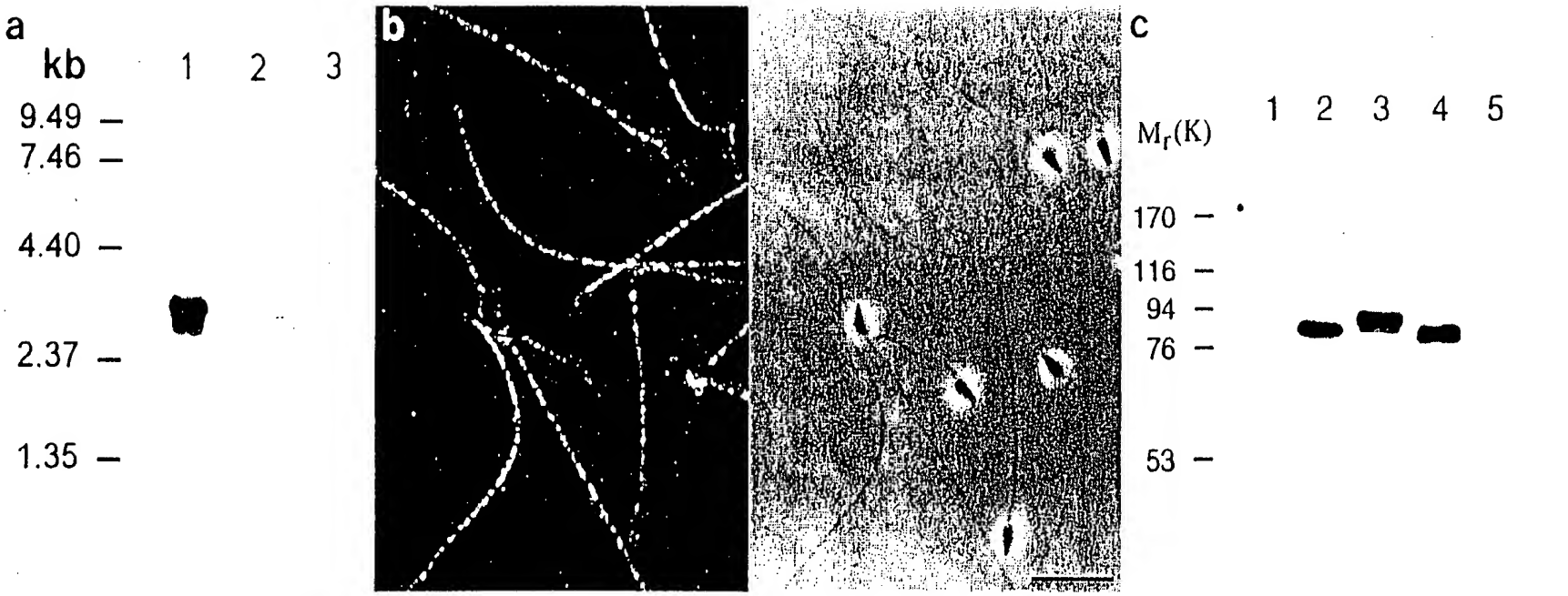

Fig. 6